```
Command line parameters:

MODEL-frame+p2n.model -DEV=soft -Q-us-09-670-568b-1 -DB=y11416.gb_pr
-MODEL-frame+p2n.model -DEV=soft -Q-us-09-670-568b-1 -DB=y11416.gb_pr
-SUFFIX-pto -OUT-=align_12 -MINMATCH-0.1 -LOOPEL-0 -LOOPEXT-0 -UNITS-bits
-START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-1 -DOCALIGN-200
-THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-1 -MODE-LOCAL -OUTFFFF-pto
-NORM-ext -HEAPSIZE-500 -MINLEM-0 -MAXLEN-200000000 -NCPUS-CORES-0 -LONGLOG -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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                                                              REFERENCE
                                                                                                                                                                                                                                                                           RESULT 1
HSY11416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen
                                                                                                                                         SOURCE
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                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                        DEFINITION
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                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                            FOCUS
FOCUS
                                          AUTHORS
                                                                                                                     ORGANISM
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq
Kaghad,M., Bonnet,H., Yang,A., Creancier,L.,
Valent,A., Minty,A., Chalon,P., Lelias,J.M.,
McKeon,F. and Caput,D.
                                                                                                                                                                                                                H.sapiens mRNA for P73.
Y11416
                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2234)
                                                                                                                   Homo sapiens
                                                                                                                                       Homo sapiens.
                                                                                                                                                           suppressor
                                                                                                                                                                         p53 transcription factor; P73 gene; transcription factor; tumor
                                                                                                                                                                                                Y11416.1 GI:2370175
                                                                                                                                                                                                                                                        HSY11416
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length:
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Ygapop 10.0 , 3
Fgapop 6.0 , 1
Delop 6.0 , 1
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2383
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Ygapext
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                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      mRNA
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                  Biscan, J.C.,
Dumont, X., 1
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PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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MEDLINE
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Direct Submission
Direct Submission
Submitted (21-FBB-1997) D. Caput, Sanofi-Elf-Bio-Rechercl
Innopole - BP 137- Voie N 1, 31676, Labege Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoallelically expressed gene related to p53 at 1p36, a region frequently deleted in neuroblastoma and other human cancers Cell 90 (4), 809-819 (1997) 97433090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9288759
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                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:015351"
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/translation="MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGG
/translation="MAQSTATSPDGGTTFEHLWSSLEPDSTYFDEHAASVPTHSPYAQP
TDSSMDVFHLEGMTTSVMAQFNLLSSYMDQMSSRAASALSYTYFDEHAASVPTHSPYAQP
SSTFDTMSPAPVIPSMTDYPGPHHFEVTFQDSSTAKSATWTYSPLLKKLKYQOIAKTCP
IQIKVSTPPPPGTAIRAMPVYKKAEHYTDVVKKCPNHELGRDPNEGQSAPASHLIVE
GNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVE
GNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFTTILYNEMCNSSCVGGMNRRPILIIIT
LEMRDGQVLGRRSFEGRICACPGRDRKADEDHYREQQALNESSAKNGAASKRAFKQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MAQSTATSPDGGTTFEHLWSSLEPDSTYFDLPQSSRGNNEVVGG
TDSSMDVFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQP
SSTFDTMSPAPVIPSNTDYPGPHHFEVTEQQSSTAKSATWTYSPLLKKLYCQIAKTCP
                                                                                                                                                                            GMLNNHGHAVPANGEMSSSHSAQSMVSGSHCTPPPPYHADPSLVRTWGP"
                                                                                                                                                                                                 PAVPALGAGVKKRRHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQ
QQLLQRPSHLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
/protein_id="CAA72219.1"
/db_xref="GI:2370177"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATISIGGSGELQRQRVMEAVHFRVRHTITIPNRGGPGGGPDEWADFGFDLPDCKARKQ
PIKEEFTEAEIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMLNNHGHAVPANGEMSSSHSAQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIEY
FTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHDYSTAQQLLRSSNA
/evidence=experimental
/protein_id="CAA72221.1"
                                                                                                                                                                                                                                                             LEMRDGQVLGRRSFEGRICACPGRDRKADEDHYREQQALNESSAKNGAASKRAFKQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQLLQRPSHLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAVPALGAGVKKRRHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="P53-like transcription factor"
/protein_id="CAA72220.1"
/db_xref="GI:2370176"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map=
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/db_xref="taxon:9606"
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                                                           /codon_start=
                                                                                   /note="second splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="first splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SPTREMBL:015350"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="allelic variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="allelic variant"
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Query Match:
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Pred. No.:
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est Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt HisIleTrpAspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPhe}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGCCCAGTCCACCGCCACC------TCCCCTGATGGGGGCACCACGTTTGAG
                                                                                                                  CCCTACACCCCAGAGCACGCCGCC---AGCGTGCCCACCCACTCGCCCTACGCACAACCC
                                                                                                                                                                                                                                                                                                              ProTyrAsnThrAspHisAlaGlnAsnSerValThrAlaProSerProTyrAlaGlnPro
                                                                                                                                                                                                                                                                                                                                                        AsnLeuGlyLeuLeuAsnSerMetAspGlnGlnIleGlnAsnGlySerSerSerThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                ATGGACGTCTTCCACCTGGAGGGCATGACTACATCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCGACCTTCCCCAGTCAAGCCGGGGGGAATAATGAGGTGGTGGGCGGAACGGATTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValAspGluProSerGluAspGlyAlaThrAsnLysIle------GluIleSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleLysValMetThrProProProGlnGlyAlaValIleArgAlaMetProValTyrLys
                                                           ATCAAGGTGTCCACCCCGCCACCCCCAGGCACTGCCATCCGGGCCATGCCTGTTTACAAG
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a 798 c
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ATPHLGPVGPCHLINNHCHAVPANGEMSSSHSAQSMVGGSHCTPBPPYHADPSLVSELT
GLGCPNCIEVFTSOGLGSIYHLQNLTIEDLGALKIPEQYEMTIWRGLQDLKQGHDYST
AQQLLRSSNAATISIGGSGELQNGRVMEAVHFRVRHTITIPNRGGPGGDDEWADFGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:015350"
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Lycqiaktcpiqikvstppppgtairampvykkaehvtdvkrcpnhelgrdfnegqs
Lycqiaktcpiqikvstppppgtairampvykkaehvtdvkrcpnhelgrdfnegqs
Lycqiaktcpiqikvstppppgtairampvykkaehvtdvkrcpnhelgrdfnegqs
Lapashlirvemnogvylgrsffergichegrdrkabedhyreqqak
NRRPLLIitlemnogvylgrsffergichegrdrkabedhyreqqak
Askrafkqsppavpalgagvkkrrhgdedtyylqvrgrenfeilmklkeslelmelyp
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Conservative:
Mismatches:
Indels:
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214

PheAsnGluGlyGlnIleAlaProProSerHisLeuIleArgValGluGlyAsnSerHis

233

멍 δÃ 밁 Ş 밁 Ş ₽ δÃ В

> 맑 δÃ Qγ δÃ Š 밁 δÃ 밁 밁 Š 닭 Ş 밁 δÃ В δÃ 밁 뮍 밁 1197 1137 1077 1017 1257 332 957 897 837 717 370 350 314 274 ValGlyGlyMetAsnArgArgProIleLeuIleIleValThrLeuGluThrArgAspGly 777 294 254 GlnValLeuGlyArgArgCysPheGluAlaArgIleCysAlaCysProGlyArgAspArg ProGlnValGlyThrGluPheThrThrValLeuTyrAsnPheMetCysAsnSerSerCys TCGCAGTATGTGGATGACCCTGTCACCGGCAGGCAGAGCGTCGTGGTGCCCTATGAGCCA AlaGlnTyrValGluAspProIleThrGlyArgGlnSerValLeuValProTyrGluPro CCACAGGTGGGGACGGAATTCACCACCATCCTGTACAACTTCATGTGTAACAGCAGCTGT GlnHisThrIleGluThrTyrArgGlnGlnGlnGln-----GlnGlnHisGlnHisLeu GGTGTGAAGAAGCGGCGCATGGAGACGAGGACACGTACTACCTTCAGGTGCGAGGCCGG SerIleLysLysArgArgSerProAspAspGluLeuLeuTyrLeuProValArgGlyArg GGGGCCGCCAGCAAGCGTGCCTTCAAGCAGAGCCCCCCTGCCGTCCCCGCCCTTGGTGCC 1136 GlyAspGlyThrLysArgProPheArgGlnAsnThrHisGlyIleGlnMet-----Thr GTAGGGGGCATGAACCGGCGGCCCATCCTCATCATCACCCCTGGAGATGCGGGATGGG 1016 1316 1256 1196 1076 836 407 389 369 349 331 313 956 293 896 273 253

Search completed: Job time : 3 secs July 7,

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FFICE
                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                            RESULT 1
HSY11416
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-SUFETX-pto -OUT--align_1_2 -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0 -UNITS-bits
-START+1 -END-1 -MATRIX-blosum62 -MINMATCH-0.1 -LOOPCL-0 -DOCALIGN-200
-THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-1 -MODE-LOCAL -OUTPMT-pto
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000 -NCPU-6 -NO_XLPXY
-NEG_SCORES-0 -LONGLOG -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                 REFERENCE
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                                                                                                                                 KEYWORDS
                                                                                                                                                  VERSION
                                                                                                                                                               ACCESSION
                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGAPOP-10 -YGAPEXT-0.5 -DELOP-6
                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                          1297.5
                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                          p53 transcription
                                                                                                                                                             H.sapiens mRNA for P73.
Y11416
 Kaghad,M., Bonnet,H., Yang,A., (
Valent,A., Minty,A., Chalon,P.,
                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                  Homo sapiens
                                                                                                                                                Y11416.1
                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic search, using
                               ammalia; Eutheria;
(bases 1 to 2234)
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2383
1 MSQSTOTNEET comm
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Ygapop
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Maximum Match 100%
Listing first 1 summaries
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Delext
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Ygapext
                                                                                                                               factor;
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                                                                                                                                                                                                                                                                                                          HSY11416
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7.0
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                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Creancier,L.,
, Lelias,J.M.,
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                                                                                                                               transcription
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Biscan, J.C.,
Dumont, X., F
                                                                                                                                                                                                                                                                                                          ACCESSION: Y11416
                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                               factor;
                                                                                                                                                                                           PRI
 Ferrara, P.,
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and Caput, D.

/codon_start=

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-FEB-1997)
Innopole - BP 137- Voie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caput, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9288759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEMRDĞQVLGRRSFEGRİCACPĞRDRKADEDHYREQQALNESSAKNGAASKRAFKQSP
PAVPALGAGVKKRRHGDEDTYYLQVRGRENFEİLMKLKESLELMELVPQPLVDSYRQQ
QQLLQRBSHLQPESYGPVLSPMNKVHGGMNKLDESVNQLVGQPEPLSGAATPNLGPVGP
GMLMNHGHAVPANGEMSSSHAQORWSGSHCTPPPPYHADBSLVSFLTGLGCPNCIEY
FTSQGLQSIYHLQNLTIEDLCALKIPEQYRMTIWRGLQDLKQGHDYSTAQQLLRSSNA
ATISIGGSGELQRQRVMEAVHERVRHTITIPNRGGPGGGPDEWADFGFDLPDCKARKQ
                                                                                                                                  GNNLSQYVDDPVTGROSVVVPYEPPQVGTEFTTILYNFMCNSSCVGGMNRRPILIIIT
LEMRDGQVLGRRSFEGRICACPGRDRKADEDHYREQQALNESSAKNGAASKRAFKQSP
PAVPALGAGVKKRRHGDEDTYYLQVRGRENFEILMKLKESLELMELVPQPLVDSYRQQ
                                                                                                                                                                                                            /db_xref="Sptrembl:015351"
/tabslation="MAQSTATSpDGGTTEHLWSSLEPDSTYFDLPQSSRGNNEVVGG
/translation="MAQSTATSpDGGTTEHLWSSLEPDSTYFDLPQSSRGNNEVVGG
TDSSMDVFHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQP
SSTEDTMSSALPUIPSMTDYOGPHHEEVTEQQSSTAKSATWTYSPLLKKLYCQIAKTCP
IQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIKEEFTEAEIH'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQIKVSTPPPPGTAIRAMPVYKKAEHVTDVVKRCPNHELGRDFNEGQSAPASHLIRVE
GNNLSQYVDDPVTGRQSVVVPYEPPQVGTEFTTILYNEMCNSSCVGGMNRRPILIIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="maqstatspdggttfehlwsslepdstyfdlpqssrgnnevvgg
TDSSMDVfHLEGMTTSVMAQFNLLSSTMDQMSSRAASASPYTPEHAASVPTHSPYAQP
SSTFDTMSPAPVIPSNTDYPGPHHFEVTFQQSSTAKSATWTYSPLLKKLYCQIAKTCP
                                                                             GMLNNHGHAVPANGEMSSSHSAQSMVSGSHCTPPPPYHADPSLVRTWGP"
                                                                                                            QQLLQRPSHLQPPSYGPVLSPMNKVHGGMNKLPSVNQLVGQPPPHSSAATPNLGPVGF
                                                                                                                                                                                                                                                                                                                                            /evidence=experimental
/protein_id="CAA72219.1"
/db_xref="GI:2370177"
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'gene="p73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_line="HT29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product="P53-like transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'cell
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'note="second splice variant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-"first splice variant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace-"t"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="allelic variant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variant"
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N 1, 31676, Labege Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        second splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanofi-Elf-Bio-Recherches, Labege
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Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us-09-670-568b-1 (1-448) x HSY11416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                         134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 ATGGACGTCTTCCACCTGGAGGGCATGACTACATCT------GTCATGGCC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 TTCGACCTTCCCCAGTCAAGCCGGGGGAATAATGAGGTGGTGGGCGGAACGGATTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 CACCTCTGGAGCTCTCTGGAACCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             537
                                                                                                                                                                                                                                                                                                                             477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 CCCTACACCCCAGAGCACGCCGCC---AGCGTGCCCACCCACTCGCCCTACGCACAACCC
                                                                                                                                         597
                                                                                                                                                                 174 IleLysValMetThrProProProGlnGlyAlaValIleArgAlaMetProValTyrLys
                                                                                                                                                                                                                                                          154 ThrTyrSerThrGluLeuLysLysLeuTyrCysGlnIleAlaLysThrCysProIleGln 173
214 PheAsnGluGlyGlnIleAlaProProSerHisLeuIleArgValGluGlyAsnSerHis 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 ProTyrAsnThrAspHisAlaGlnAsnSerValThrAlaProSerProTyrAlaGlnPro 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 AsnLeuGlyLeuLeuAsnSerMetAspGlnGlnIleGlnAsnGlySerSerSerThrSer 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 MetAspCysIleArgMetGlnAspSerAspLeuSerAspProMetTrpProGlnTyrThr 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 HisileTrpAspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPhe 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGlu------ValPheGln 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValAspGluProSerGluAspGlyAlaThrAsnLysIle------GluIleSer 53
                                                                                                                                                                                                                                                                                                                           GlyProHisSerPheAspValSerPheGlnGlnSerSerThrAlaLysSerAlaThrTrp 153
                                                                                                                                                                                                                                                                                                                                                                                                                    SerSerThrPheAspAlaLeuSerProSerProAlaIleProSerAsnThrAspTyrPro 133
                                                                                                                                                                                                                                  ACGTACTCCCCGCTCTTGAAGAAACTCTACTGCCAGATCGCCAAGACATGCCCCATCCAG
                                                                                                                                         ATCAAGGTGTCCACCCCGCCACCCCCAGGCACTGCCATCCGGGCCATGCCTGTTTACAAG
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VPTHSYAQPSSTEDTMSPAPVIEWTSVWAQFNLLSSTMDQMSSRAASASPYTPEHAAS
VPTHSYAQPSSTEDTMSPAPVIEWTYKKAEHVTDVKRCPHELGRDENEGQS
APASHLIRVEGINILSQYVDDPVTGRQSVVVPYEBPQVCTEFTTILYNKHCNSSCVGGM
RREPLIJIITLEMRDGQVLGRRSFEGRICACPGRDKKADEDHYREQQALMESSAKNGA
ASKRAFKQSPPAVPALGAGVKKRRHGDEDTYYLQVRGKENFEILMKLKESLELMELVP
QPLVDSYRQQQQLLQRESHLQPPSYGPVLSPMKVHGGMNKLPSVNQLVGQPPPHSSA
ATPHLEPVFGYRQGQOLLQRESHLQPPSYGPVLSPMKVHGGMNKLPSVNQLVGQPPPHSSA
ATPHLEPVFGYRQGQOLLQRESHLQPPSYGPVLSPMKVHGGMNKLFSHPQLFGFYBSA
ATPHLEPVFGYGGLASIYHLQNLTIEDLGALKIPEQYRHTIWRGLADFGFTGGGLQSIYHLQNLTIEDLGALKIPEQYRHTIWRGLADFGFTGGLCCPNCIEWTSGGLQSIYHLQNLTIEDLGALKIPEQYRHTITIPHRGGPGGGPDEWADFGF
AQQLLRSSNAATISIGGSGELOKGRVEAVHFRVRHTITIPHRGGPGGGPDEWADFGF
AQQLLRSSNAATISIGGSTEAEIH*
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